

IN THE CLAIMS

The status of the claims of the present application is listed below:

Claims 1-69: Canceled.

70. (Previously Presented): An isolated DNA coding for a polypeptide which comprises the amino acid sequence of SEQ ID NO: 1, 2 or 3.

71. (Previously Presented) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 1.

72. (Previously Presented) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

73. (Previously Presented) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 3.

74. (Previously Presented) A vector comprising the DNA of Claim 70.

75. (Previously Presented) The vector of Claim 74, which is a plasmid.

76. (Previously Presented) A plant transformed with the DNA of Claim 70.

77. (Currently Amended) The plant of Claim 76, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), ~~cotton (*Gossypium*)~~ cotton (*Gossypium hirsutum*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

78. (Previously Presented) The plant of Claim 76, wherein the plant is a dicotyledonous plant.

79. (Previously Presented) The plant of Claim 78, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodicaceae*, or *Gramineae* plant.

80. (Previously Presented) The plant of Claim 79, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

81. (Previously Presented) A plant transformed with the vector of Claim 74.

82. (Currently Amended) The plant of Claim 81, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), ~~cotton (*Gossypium*)~~ cotton (*Gossypium hirsutum*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

83. (Previously Presented) The plant of Claim 81, wherein the plant is a dicotyledonous plant.

84. (Previously Presented) The plant of Claim 83, wherein the plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodicaceae*, or *Gramineae* plant.

85. (Previously Presented) The plant of Claim 83, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

86. (Previously Presented) A host cell transformed with the DNA of Claim 70.

87. (Previously Presented) The host cell of Claim 86, which is a prokaryotic or a eukaryotic cell.

88. (Previously Presented) The host cell of Claim 86, which is a bacterial cell.

89. (Previously Presented) The host cell of Claim 86, which is a plant cell.

90. (Previously Presented) The host cell of Claim 86, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane cell.

91. (Previously Presented) A chimeric gene comprising the DNA of Claim 70 operably linked to a transcription regulatory region expressible in plant cells.

92. (Previously Presented) A plant transformed with the chimeric gene of Claim 91.

93. (Previously Presented) The plant of Claim 92, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

94. (Previously Presented) A method of modifying the content of raffinose family oligosaccharides in a plant, comprising transforming a plant with the chimeric gene of Claim 91, thereby changing the content of raffinose family oligosaccharides in the plant.

95. (Previously Presented) The method of Claim 94, wherein the plant is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

96. (Previously Presented) A method of producing a polypeptide which comprises an amino acid sequence of SEQ ID NO: 1, 2 or 3, comprising culturing the host cell of Claim 90 under conditions where said polypeptide is expressed, and isolating said polypeptide.

97. (Previously Presented): An isolated DNA molecule encoding a polypeptide having an ability to produce raffinose from sucrose and galactinol, wherein the DNA is hybridizable under stringent conditions to a DNA comprising nucleotide numbers 56 to 2407 of SEQ ID NO: 4, the stringent conditions being 1X SSC, 0.1% SDS at 60°C, wherein the polypeptide having the ability to produce raffinose from sucrose and galactinol has the following properties:

- (1) optimum pH: the polypeptide has an optimum pH of about 6 to 8;
- (2) optimum temperature: the polypeptide has an optimum temperature of about 35 to 40°C;
- (3) molecular weight: the polypeptide has:
 - (i) a molecular weight of about 75 kDa to 95 kDa estimated by gel filtration chromatography;
 - (ii) a molecular weight of about 90 kDa to 100 kDa estimated by polyacrylamide gel electrophoresis; and

(iii) a molecular weight of about 90 kDa to 100 kDa estimated by SDS-polyacrylamide gel electrophoresis under a reduced condition; and

(4) inhibition: the polypeptide is inhibited by iodoacetamide, N-ethylmaleimide, and myo-inositol.

98. (Previously Presented) A vector comprising the DNA of Claim 97.

99. (Previously Presented) The vector of Claim 98, which is a plasmid.

100. (Previously Presented) A plant transformed with the DNA of Claim 97.

101. (Currently Amended) The plant of Claim 100, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), ~~cotton (*Gossypium*)~~ cotton (*Gossypium hirsutum*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

102. (Previously Presented) The plant of Claim 101, wherein the plant is a dicotyledonous plant.

103. (Previously Presented) The plant of Claim 102, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.

104. (Previously Presented) The DNA of Claim 102, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

105. (Previously Presented) A plant transformed with the vector of Claim 98.

106. (Currently Amended) The plant of Claim 105, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), ~~cotton (*Gossypium*)~~ cotton (*Gossypium hirsutum*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

107. (Previously Presented) The plant of Claim 105, wherein the plant is a dicotyledonous plant.

108. (Previously Presented) The plant of Claim 107, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.

109. (Previously Presented) The DNA of Claim 107, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

110 (Previously Presented) A host cell transformed with the DNA of Claim 97.

111. (Previously Presented) The host cell of Claim 110, which is a prokaryotic or a eukaryotic cell.

112. (Previously Presented) The host cell of Claim 110, which is a bacterial cell.

113. (Previously Presented) The host cell of Claim 110, which is a plant cell.

114. (Previously Presented) The host cell of Claim 110, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane cell.

115. (Previously Presented) A chimeric gene comprising the DNA of Claim 97 operably linked to a transcription regulatory region expressible in plant cells.

116. (Previously Presented) A plant transformed with the chimeric gene of Claim 115.

117. (Previously Presented) The plant of Claim 116, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

118. (Previously Presented) A method of modifying the content of raffinose family oligosaccharides in a plant, comprising transforming a plant with the chimeric gene of Claim 115, thereby changing the content of raffinose family oligosaccharides in the plant.

119. (Previously Presented) The method of Claim 118, wherein the plant is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

120. (Previously Presented) A method of producing a polypeptide comprising culturing the host cell of Claim 110 under conditions where said polypeptide is expressed, and isolating said polypeptide.